AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph that begins on line 23, page 8, with the following corrected paragraph:

For purposes of comparing two different nucleic acid or polypeptide sequences, one sequence (comparing sequence) may be described to be a specific "percent identical to" another sequence (reference sequence) in the present disclosure. In this respect, the percentage identity is determined by the algorithm of Karlin and Altschul, Proc. Natl. Acad. Sci. USA, 90:5873-5877 (1993), which is incorporated into the various BLAST programs. Specifically, the percentage identity is determined by the "BLAST 2 Sequences" tool, which is available on the world wide web at ncbi.nlm.nih.gov. ~~through the National Center for Biotechnology Information, National Library of Medicine, Building 38A, Bethesda, MD 20894~~. See Tatusova and Madden, FEMS Microbiol. Lett., 174(2):247-250 (1999). For pairwise DNA-DNA comparison, the BLASTN 2.1.2 program is used with default parameters (Match: 1; Mismatch: -2; Open gap: 5 penalties; extension gap: 2 penalties; gap x_dropoff: 50; expect: 10; and word size: 11, with filter). For pairwise protein-protein sequence comparison, the BLASTP 2.1.2 program is employed using default parameters (Matrix: BLOSUM62; gap open: 11; gap extension: 1; x_dropoff: 15; expect: 10.0; and wordsize: 3, with filter).

Please replace the paragraph that begins on line 21, page 44, with the following corrected paragraph:

The specific features of siRNAs required for inducing the efficient degradation or silencing of corresponding RNA transcripts have been systematically investigated, as have the features of the target sequence within the targeted transcript. The results of such experiments have been published and general guideline have been established for the design of effective siRNA molecules (see: Tuschl et al., Genes & Dev. 13:3191-3197 (1999) and Elbashir et al., EMBO J. 20:6877-6888 (2001), and discussions in "The siRNA User Guide" ~~which was incorporated into Elbashir, et al., Methods 26:199-213 (2002) and is available from the Tuschl Laboratory, Laboratory of RNA Molecular Biology, Rockefeller University, 1230 York Avenue, Box 186, New York, NY 10021~~.